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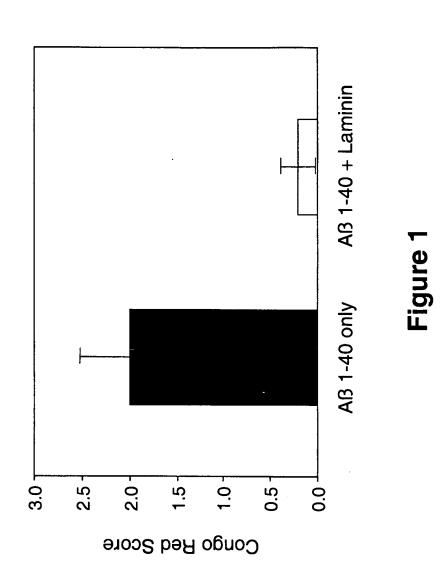
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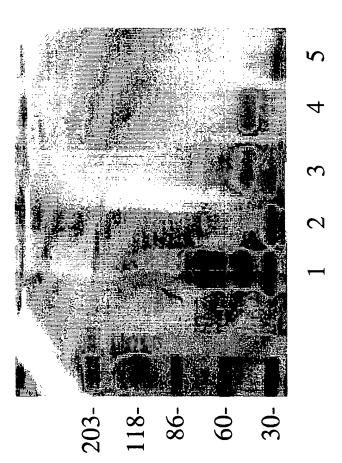
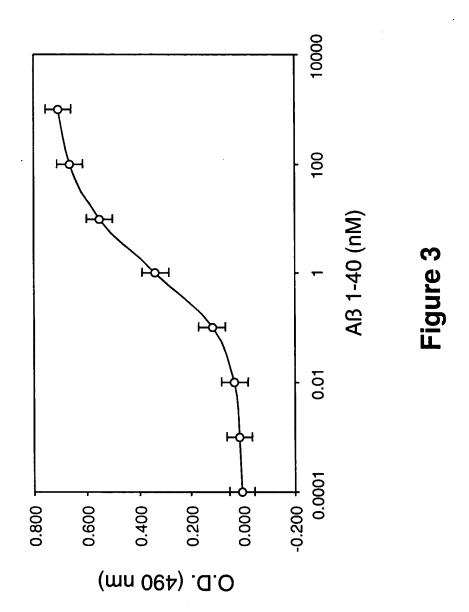


Figure 2



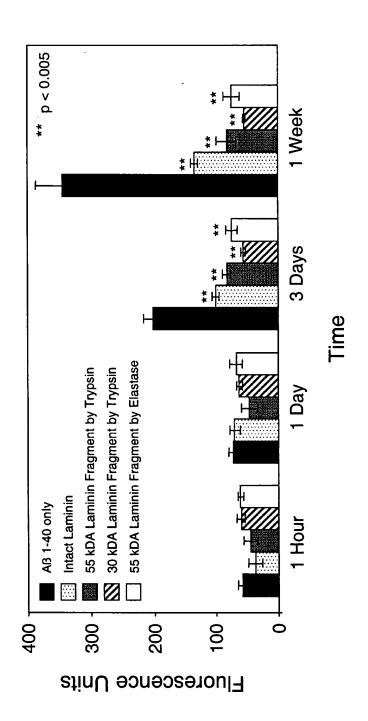


Figure 4

TKTFRINQLLQDTPVASPRSVKVWQDACSPLPKTQANHGALQFGDIPTSH 1376 ALGTDGKKLRIKSKEKCNDGKWHTVVFGHDGEKGRLVVDGLRAREGSLPG 1476 1127 VVRLNDTVGVTKKCSEDWKLVRSASFSRGGQLSFTDLGLPPTDHLQASFG 1176  $^{1177}$  FQTFQPSGILLDHQTWTRNLQVTLEDGYIELSTSDSGGPIFKSPQTYMDG  $^{1226}$ LLHYVSVISDNSGLRLLIDDQLLRNSKRLKHISSSRQSLRLGGSNFEGCI 1276 SNVFVQRLSLSPEVLDLTSNSLKRDVSLGGCSLNKPPFLMLLKGSTRFNK 1326 1377 LLFKLPQELLKPRSQFAVDMQTTSSRGLVFHTGTKNSFMALYLSKGRLVF 1426 NSTISIRAPVYLGSPPSGKPKSLPTNSFVGCLKNFQLDSKPLYTPSSSFG 1528 A3G50 A3G74 A3G80 A3G48 A3G85 A3G60 A3G67 A3G41 VSSCLGGPLEKGIYFS 1542 A3G53 A3G84 1227 1327 1427 1477 1527 1277

Figure 5

```
TSISLYMKPPPKPOTTGAWVADQFVLYLGSKNAKKEYHGLAIKNDNLVYVYNLGHKDVEILLDSKPVSSWPAYFSTV
A4G-1 A4G-2 A4G-3 A4G-4 A4G-5 A4G-6 A4G-7 A4G-8 A4G-9 A4G-10
XIERVGKHGKVFLTVPSSSSTAEEKFIKKGEFAGDDSLLDLTPEDTVFYVGGVPANFKLPASLNLPSYSGCLELATL

A4G-11 A4G-12 A4G-13 A4G-14 A4G-15 A4G-16 A4G-17 A4G-18 A4G-19
1006
NNDVISLYNFKHIYNMDPSKSVPCARDKLAFTQSRAASYFFDGSSYAVVRDITRRGKFGQVTRFDIEIRTPADNGLV
A4G-20 A4G-21 A4G-22 A4G-23 A4G-24 A4G-25 A4G-26 A4G-27 A4G-28
LLMVNGSMFFSLEMRNGYLHVFYDFGFSNGPVHLEDTLKKAQINDAKYREISIIYHNDKKMILVVDRRHVKSTDNEK

A4G-29 A4G-30 A4G-31 A4G-32 A4G-33 A4G-34 A4G-35 A4G-36 A4G-37
11160
KKIPFTDIYIGGAPQEVLQSRTLRAHLPLDINFRGCMKGIQFQKKDFMLLEQTETLGVGYGCPEDSLISRRAYFNGQ
A4G-38 A4G-39 A4G-40 A4G-41 A4G-42 A4G-43 A4G-44 A4G-45 A4G-46 A4G-47
SFIASIQKISFFDGFEGGFNFRTLOPNGLLFYYTSGSDVFSISLDNGTVVMDVKGIKVMSTDKQYHDGLPHFVVTSI

A4G-48 A4G-49 A4G-50 A4G-51 A4G-52 A4G-53 A4G-54 A4G-55 A4G-56
1314
SDTRYELVVDKSRLRGKNPTKGKAEQTOTTEKKFYFGGSPISPQYANFTGCISNAYFTRLDRDVEVEAFQRYSEKVH
 A4G-57 A4G-58 A4G-59 A4G-60 A4G-61 A4G-62 A4G-63 A4G-64 A4G-65 A4G-66
1391
TSLYECPIESSPLFLLHKXGKNSSKPKTNKQGEKSKDAPSWDPIGLKFLEQKAPRDSHCHLFSSPRAIEHAYQYGGT
 A4G-67 A4G-68 A4G-69 A4G-70 A4G-71 A4G-72 A4G-73 A4G-74 A4G-75
 1646
Ansrqefeheggdfgeksgfsirlktrsshgmifyvsdqeendfhtlflahgrlvfmfnvghkklkirsqekyndgl
 A4G-76 A4G-77 A4G-78 A4G-79 A4G-80 A4G-81 A4G-82 A4G-83 A4G-84 A4G-85
 1545
WHDVIFIREKSSGRLVIDGLRVLBERLPPSGAAWKIKGPIYLGGVAPGRAVKNVQITSVYSFSGCLGNLQLNGASIT
 A4G-86 A4G-87 A4G-88 A4G-89 A4G-90 A4G-91 A4G-92 A4G-93
 1622
SASQTPSVTPCFEGPMETGTYPSTEGGYVVLDESFNIGLKFEIAPEVRPRSSSGTLVHGHSVNGEYLNVHHRNGQVI
  A4G-95 A4G-97 A4G-98 A4G-99 A4G-100 A4G-101 A4G-102 A4G-103
 1699
VKVNNGVRDFSTSVTPKQNLCDGRWHRITVIRDSNVVQLDVDSEVNHVVGPLNPKPVDHREPVFVGGVPESLLTPRL
  A4G-104 A4G-105 A4G-106 A4G-107 A4G-108 A4G-109 A4G-110 A4G-111 A4G-112
 1776
APSKPFTGCIRHFVIDSRPVSFSKAALVSGAVSINSCPTA
  A4G-113 A4G-114 A4G-115 A4G-116
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Figure 6

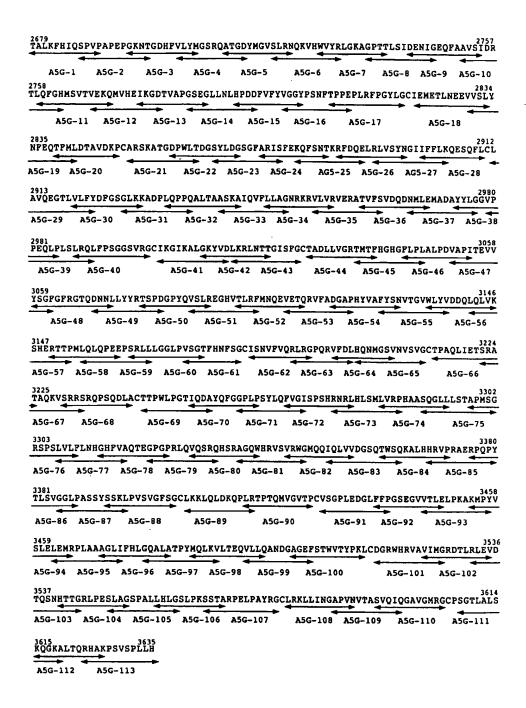
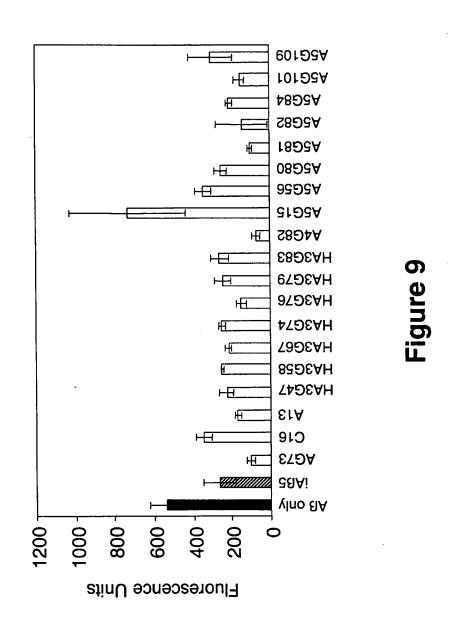


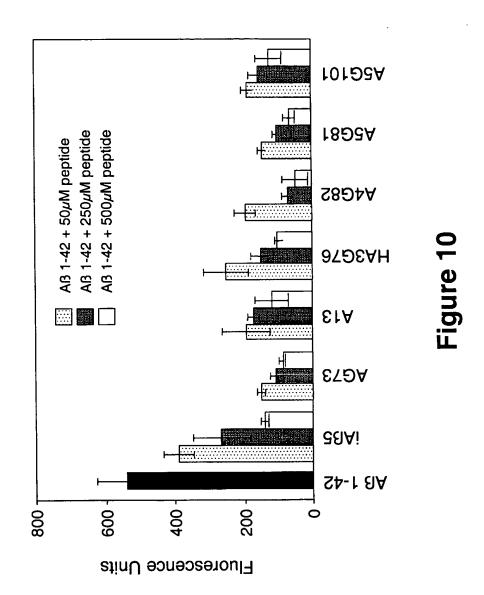
Figure 7

PEPTIDES	Laminin Chain and Amino Acid Sequence Number	Amino Acid Sequence	% Disruption/ Disassembly of Fibrillar AB (AB:Peptide Molar Ratio of 1:6)
AG73	Alpha-1 chain; residues 2719-2730	RKRLQVQLSIRT	46 % (S; p < 0.01)***
A3	Alpha-3 chain; residues 2243-2254	KPRLQFSLDIQT	23 % (S; p < 0.01)
A5	Alpha-5 chain; residues 3275-3286	RNRLHLSMLVRP	22 % (S; p<0.01)
C-16	Gamma-1 chain; residues 139-150	KAFDITYVRLKF	28 % (S; p<0.01)***
LAM-L	Alpha-1 chain; residues 2097-2108	AASIKVAVSADR	24 % (S; p<0.01)
A-13	Alpha-1 chain; residues 97-109	RQVFQVAYIIIKA	30 % (S; p<0.01)***
HA3G45	Alpha-3 chain, residues 1173-1184	ASFGFQTFQPSG	21 % (S; p<0.05)
HA3G47	Alpha-3 chain; residues 1189-2000	HQTWTRNLQVTL	28 % (S; p<0.01)***
HA3G58	Alpha-3 chain; residues 1276-1287	ISNVFVQRLSLS	32 % (S; p<0.01)***
HA3G67	Alpha-3 chain; residues 1342-1353	ASPPSVKVWQDA	25 % (S; p<0.01)***
HA3G71	Alpha-3 chain; residues 1379-1390	FKLPQELLKPRS	23 % (S; p<0.05)
HA3G74	Alpha-3 chain; residues 1402-1414	RGLVFHTGTKNSF	32 % (S; p<0.01)***
HA3G75	Alpha-3 chain; residues 1411-1422	KNSFMALYLSKG	24 % (S; p<0.01)
HA3G76	Alpha-3 chain; residues 1418-1429	YLSKGRLVFALG	26 % (S; p<0.01)***
HA3G79	Alpha-3 chain; residues 1444-1455	NDGKWHTVVFGH	27 % (S; p<0.01)***
HA3G83	Alpha-3 chain; residues 1477-1487	GNSTISIRAPVY	33 % (S; p<0.01)***
A4G31	Alpha-4 chain; residues 1101-1112	LHVFYDFGFSNG	23 % (S; p<0.01)
A4G82	Alpha-4 chain; residues 1513-1524	TLFLAHGRLVFM	30 % (S; p<0.01)***
A5G15	Alpha-5 chain; residues 2792-2803	HPDDFVFYVGGY	30 % (S; p<0.01)***
A5G35	Alpha-5 chain; residues 2950-2961	VLVRVERATVFS	20 % (S; p<0.05)
A5G46	Alpha-5 chain; residues 3043-3054	FLPLALPDVAPI	21 % (S; p<0.05)
A5G56	Alpha-5 chain; residues 3135-3146	WLYVDDQLQLVK	27 % (S; p<0.01)***
A5G71	Alpha-5 chain; residues 3259-3270	GPLPSYLQFVGI	22 % (S; p<0.05)
A5G80	Alpha-5 chain; residues 3329-3340	VQSRQHSRAGQW	25 % (S; p<0.01)***
A5G81	Alpha-5 chain; residues 3337-3348	AGQWHRVSVRWG	41 % (S; p<0.01)***
A5G82	Alpha-5 chain; residues 3345-3356	VRWGMQQIQLVV	29 % (S; p<0.01)***
A5G84	Alpha-5 chain; residues 3361-3372	TWSQKALHHRVP	27 % (S; p<0.01)***
A5G101	Alpha-5 chain; residues 3516-3527	DGRWHRVAVIMG	39 % (S; p<0.01)***
A5G109	Alpha-5 chain; residues 3587-3598	APVNVTASVQIQ	32 % (S; p<0.01)***
A5G110	Alpha-5 chain; residues 3594-3605	SVQIQGAVGMRG	23 % (S; p<0.05)

<sup>\*\*\*</sup> Selected for Further Testing

Figure 8





PTI-	Structure	Formula	MW
DP-001 D-AG73 or D-A1 A1-chain 2719-2730	Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr	C <sub>64</sub> H <sub>120</sub> N <sub>24</sub> O <sub>17</sub>	1497.82
DP-002 D-A13 A1-chain 97-109	Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala	C74H121N19O17	1548.90
DP-003 D-HA3G76 A3-chain 1418-1429	Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly	C <sub>63</sub> H <sub>102</sub> N <sub>16</sub> O <sub>15</sub>	1323.61
DP-004 D-A4G82 A4-chain 1513-1524	Thr-Leu-Phe-Leu-Ala-His-Gly-Arg-Leu-Val-Phe-Met	C <sub>67</sub> H <sub>105</sub> N <sub>17</sub> O <sub>14</sub> S	1404.75
DP-005 D-A5G81 A5-chain 3337-3348	Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly	C <sub>65</sub> H <sub>95</sub> N <sub>23</sub> O <sub>15</sub>	1438.62
DP-006 D-A5G101 A5-chain 3516-3527	Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly	C <sub>61</sub> H <sub>97</sub> N <sub>21</sub> O <sub>15</sub> S	1396.65
DP-007 D-HA3G47 A3-chain 1189-2000	His-Gln-Thr-Trp-Thr-Arg-Asn-Leu-Gln-Val-Thr-Leu	C <sub>66</sub> H <sub>105</sub> N <sub>21</sub> O <sub>19</sub>	1496.70
DP-008 D-HA3G58 A3-chain 1276-1287	Ile-Ser-Asn-Val-Phe-Val-Gln-Arg-Leu-Ser-Leu-Ser	C <sub>61</sub> H <sub>103</sub> N <sub>17</sub> O <sub>18</sub>	1362.60

Fig. 12a

PTI-	I	Structure	Formula	MW
DP-009 D-HA3G74 A3-chain 1402-1414	A	Arg-Gly-Leu-Val-Phe-His-Thr-Gly-Thr-Lys-Asn-Ser-Phe	C <sub>66</sub> H <sub>102</sub> N <sub>20</sub> O <sub>18</sub>	1463.67
DP-010 D-HA3G83 A3-chain 1477-1487		Gly-Asn-Ser-Thr-Ile-Ser-Ile-Arg-Ala-Pro-Val-Tyr	C <sub>56</sub> H <sub>92</sub> N <sub>16</sub> O <sub>18</sub>	1277.45
DP-011 D-A5G82 A5-chain 3345-3356		Val-Arg-Trp-Gly-Met-Gln-Gln-Ile-Gln-Leu-Val-Val	C <sub>66</sub> H <sub>109</sub> N <sub>19</sub> O <sub>16</sub> S	1456.78
DP-012 D-A5G109 A3-chain 1444-1455		Ala-Pro-Val-Asn-Val-Thr-Ala-Ser-Val-Gln-Ile-Gln	C53H91N15O18	1226.40
DP-013 D-rAG73 or D-rA1 A1-chain r2719-2730 or 2730-2719		Thr-Arg-Ile-Ser-Leu-Gln-Val-Gln-Leu-Arg-Lys-Arg	C <sub>64</sub> H <sub>120</sub> N <sub>24</sub> O <sub>17</sub>	1497.82
DP-014 D-rA13 Al-chain r92-109 or 109-92		Ala-Lys-Ile-Ile-Ile-Tyr-Ala-Val-Gln-Phe-Val-Gln-Arg	C74H121N19O17	1547.92
DP-015 D-rHA3G76 A3-chain r1418-1429 or 1429-1418		Gly-Leu-Ala-Phe-Val-Leu-Arg-Gly-Lys-Ser-Leu-Tyr	C <sub>63</sub> H <sub>102</sub> N <sub>16</sub> O <sub>15</sub>	1323.61
DP-016 D-rA4G82 A4-chain r1513-1524 or 1524-1513		Met-Phe-Val-Leu-Arg-Gly-His-Ala-Leu-Phe-Leu-Thr	C <sub>67</sub> H <sub>105</sub> N <sub>17</sub> O <sub>14</sub> S	1404.75

Fig. 12b

PTI-		Structure	Formula	MW
DP-017 D-rA5G81 A5-chain r3337-3348 or 3348-3337		Gly-Trp-Arg-Val-Ser-Val-Arg-His-Trp-Gln-Gly-Ala	C <sub>65</sub> H <sub>95</sub> N <sub>23</sub> O <sub>15</sub>	1438.62
DP-018 D-rA5G101 A5-chain r3516-3527 or 3527-3516	· ·	Gly-Met-Ile-Val-Ala-Val-Arg-His-Trp-Arg-Gly-Asp	C <sub>61</sub> H <sub>97</sub> N <sub>21</sub> O <sub>15</sub> S	1396.65
LP-019 AG73 or A1 A1-chain 2719-2730		Arg-Lys-Arg-Lue-Gln-Val-Gln-Leu-Ser-Ile-Arg-Thr	C <sub>64</sub> H <sub>120</sub> N <sub>24</sub> O <sub>17</sub>	1497.82
LP-020 A13 A1-chain 92-109		Arg-Gln-Val-Phe-Gln-Val-Ala-Tyr-Ile-Ile-Ile-Lys-Ala	C74H121N19O17	1548.90
LP-021 HA3G76 A3-chain 1418-1429		Tyr-Leu-Ser-Lys-Gly-Arg-Leu-Val-Phe-Ala-Leu-Gly	C <sub>63</sub> H <sub>102</sub> N <sub>16</sub> O <sub>15</sub>	1323.61
LP-022 A4G82 A4-chain 1513-1524	r.	Thr-Leu-Phe-Phe-Met-Arg-Leu-Val-His-Ala-Leu-Gly	C <sub>67</sub> H <sub>105</sub> N <sub>17</sub> O <sub>14</sub> S	1404.75
LP-023 A5G81 A5-chain 3337-3348		Ala-Gly-Gln-Trp-His-Arg-Val-Ser-Val-Arg-Trp-Gly	C <sub>65</sub> H <sub>95</sub> N <sub>23</sub> O <sub>15</sub>	1438.62
LP-024 A5G101 A5-chain 3516-3527		Asp-Gly-Arg-Trp-His-Arg-Val-Ala-Val-Ile-Met-Gly	C <sub>61</sub> H <sub>97</sub> N <sub>21</sub> O <sub>15</sub> S	1396.65

Fig. 12c

PTI-	Structure	Formula	MW
LP-025  β-sheet breaker or iAβ5	Leu-Pro-Phe-Asp	C <sub>33</sub> H <sub>43</sub> N <sub>5</sub> O <sub>8</sub>	637.74
DP-026 Trc'n 5;1-7	Ala-Gly-Gln-Trp-His-Arg-Val	C <sub>38</sub> H <sub>56</sub> N <sub>14</sub> O <sub>9</sub>	852.95
DP-027 Trc'n 5;2-8	Gly-Gln-Trp-His-Arg-Val-Ser	C <sub>38</sub> H <sub>56</sub> N <sub>14</sub> O <sub>10</sub>	868.95
DP-028 Trc'n 5;3-9	Gln-Trp-His-Arg-Val-Ser-Val	C <sub>41</sub> H <sub>62</sub> N <sub>14</sub> O <sub>10</sub>	911.04
DP-029 Trc'n 5;4-10	Trp-His-Arg-Val-Ser-Val-Arg	C <sub>42</sub> H <sub>66</sub> N <sub>16</sub> O <sub>9</sub>	939.09
DP-030 Trc'n 5;5-11	His-Arg-Val-Ser-Val-Arg-Trp	C <sub>42</sub> H <sub>66</sub> N <sub>16</sub> O <sub>9</sub>	939.09
DP-031 Tre'n 5;6-12	Arg-Val-Ser-Val-Arg-Trp-Gly	C <sub>38</sub> H <sub>62</sub> N <sub>14</sub> O <sub>9</sub>	859.00
DP-032 Trc'n 6;1-7	Asp-Gly-Arg-Trp-His-Arg-Val	C <sub>40</sub> H <sub>60</sub> N <sub>16</sub> O <sub>10</sub>	925.02

Fig. 12d

PTI-		Structure	Formula	MW .
DP-033	T	Gly-Arg-Trp-His-Arg-Val-Ala		
Trc'n 6;2-8		HO AND HOLL MAN THE	C <sub>39</sub> H <sub>60</sub> N <sub>16</sub> O <sub>8</sub>	881.01
DP-034 Trc'n 6;3-9		Arg-Trp-His-Arg-Val-Ala-Val	C <sub>42</sub> H <sub>66</sub> N <sub>16</sub> O <sub>8</sub>	923.09
DP-035 Trc'n 6;4-10		Trp-His-Arg-Val-Ala-Val-Ile	 C <sub>42</sub> H <sub>65</sub> N <sub>13</sub> O <sub>8</sub>	880.07
DP-036 Trc'n 6;5-11		His-Arg-Val-Ala-Val-Ile-Met	C <sub>36</sub> H <sub>64</sub> N <sub>12</sub> O <sub>8</sub> S	825.05
DP-037 Trc'n 6;6-12	·	Arg-Val-Ala-Val-Ile-Met-Gly	C <sub>32</sub> H <sub>60</sub> N <sub>10</sub> O <sub>8</sub> S	744.96
DP-038 Trc'n 4;1-7		Thr-Leu-Phe-Leu-Ala-His-Gly	C <sub>36</sub> H <sub>55</sub> N <sub>9</sub> O <sub>9</sub>	757.89
DP-039 Trc'n 4;2-8		Leu-Phe-Leu-Ala-His-Gly-Arg	C <sub>38</sub> H <sub>60</sub> N <sub>12</sub> O <sub>8</sub>	812.97
DP-040 Trc'n 4;3-9		Phe-Leu-Ala-His-Gly-Arg-Leu  HSA - His-Gly-Arg-Leu  HSA - His-Gly-Ar	C <sub>38</sub> H <sub>60</sub> N <sub>12</sub> O <sub>8</sub>	812.98

Fig. 12e

PTI-		Structure	Formula	MW
DP-041	-	Leu-Ala-His-Gly-Arg-Leu-Val		
Trc'n	-	but had I I I		
4;4-10		191 191 191 191 COH	C <sub>34</sub> H <sub>60</sub> N <sub>12</sub> O <sub>8</sub>	764.93
	1		1	
		los nots		
DD 042		Ala-His-Gly-Arg-Leu-Val-Phe	<del> </del>	
DP-042 Trc'n		Ala-Mis-Oly-Alg-Leu-Val-Mic	, ,	
4;5-11			C <sub>37</sub> H <sub>58</sub> N <sub>12</sub> O <sub>8</sub>	798.95
7,5-11		0 5 7 7 0	03/22382 112 08	,,,,,,
	_	101 - 101		
DP-043		His-Gly-Arg-Leu-Val-Phe-Met		
Trc'n			C <sub>39</sub> H <sub>62</sub> N <sub>12</sub> O <sub>8</sub> S	859.07
4;6-12			C391 1621 V12 C83	659.07
·				-
DP-044	·	Gly-Leu-Ala-Phe-Val-Leu-Arg		
Trc'n				
15;1-7		1012	$C_{37}H_{62}N_{10}O_8$	774.97
•				
		-		
DP-045	·	Leu-Ala-Phe-Val-Leu-Arg-Gly		
Trc'n			C <sub>37</sub> H <sub>62</sub> N <sub>10</sub> O <sub>8</sub>	774.97
15;2-8		\ \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	C3711621110O8	
		1		
DP-046		Ala-Phe-Val-Leu-Arg-Gly-Lys		
Trc'n	İ			
15;3-9		TOTAL	C <sub>37</sub> H <sub>63</sub> N <sub>11</sub> O <sub>8</sub>	789.98
		in the same same		
DP-047	†	Phe-Val-Leu-Arg-Gly-Lys-Ser		
Trc'n				
15;4-10		MAT AND	$C_{37}H_{63}N_{11}O_9$	805.98
		HO NOTE WITH		
DP-048	†	Val-Leu-Arg-Gly-Lys-Ser-Leu		·
Trc'n	•			
15;5-11	1	NH NH NH NH OH	C <sub>34</sub> H <sub>65</sub> N <sub>11</sub> O <sub>9</sub>	771.96
,			34 03 11	
		HN N		
		MN NH <sub>2</sub>	1	
DP-049	T	Leu-Arg-Gly-Lys-Ser-Leu-Tyr		
Trc'n				
15;6-2		HON THE TOUR MALE WASH	$C_{38}H_{65}N_{11}O_{10}$	836.01
		1		
		100		
	1	Fig. 12f		L

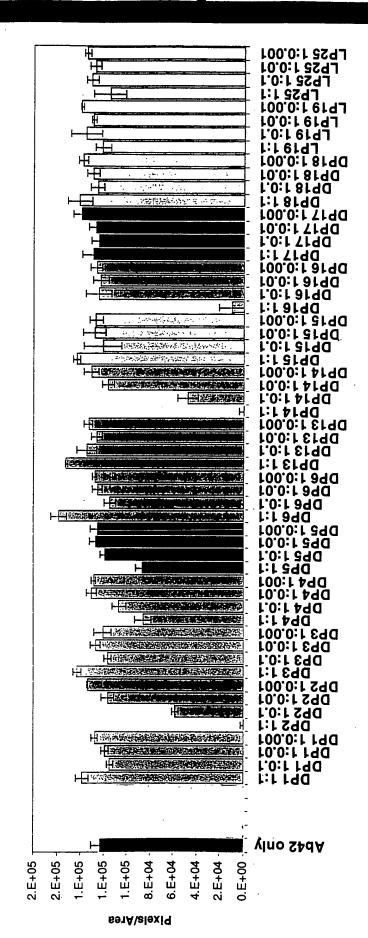
Fig. 12f

aminin Peptides

Vitro Screening of

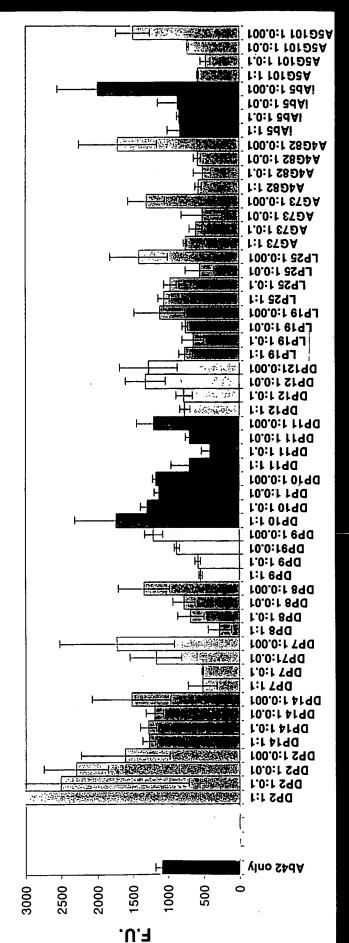
# Vitro Screening of Laminin Peptides

Congo Red Binding of Ab42 +/- Laminin Peptides



## aminin Peptides n Vitro Screening of

**ThioT** 



## Laminin Peptides Vitro Screening of

